

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2002, 06:38:56 ; Search time 1709.21 Seconds
(without alignments)
2605.879 Million cell updates/sec

Title: US-09-622-613A-14

Perfect score: 330
Sequence: 1 cagaactggcacttcca.....ctggtatcggtcgtgcccg 330

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	40	12.1	500	9	AU087262 AU087262
C 2	39.2	11.9	565	9	AA481151 aa34f11.s
C 3	39.2	11.9	1014	10	B1948321 HVSME1000
C 4	38.2	11.6	1067	12	CNS00C08
C 5	38	11.5	914	12	AZ205202
C 6	37.8	11.5	590	10	AZ205202
C 7	37.6	11.4	655	10	B1814232
C 8	37	11.2	530	12	BG590791
C 9	36.8	11.2	514	9	AV441651
C 10	36.8	11.2	558	12	AZ729728
C 11	36.8	11.2	709	12	AZ729728
C 12	36.4	11.0	428	12	AZ161580
C 13	36.4	11.0	644	12	AQ365154
C 14	36.4	11.0	739	12	AZ196614
C 15	36.2	11.0	561	12	AZ841683
C 16	36.2	11.0	652	12	AM690825
C 17	36	10.9	853	12	CNS023KH

C 18	36	10.9	918	12	CNS03XDD
C 19	35.8	10.8	425	12	A1176919
C 20	35.8	10.8	544	9	AM299150
C 21	35.8	10.8	604	9	BE204104
C 22	35.8	10.8	628	9	BE204201
C 23	35.8	10.8	644	9	BE202886
C 24	35.8	10.8	720	9	BE202887
C 25	35.8	10.8	1025	12	A2547484
C 26	35.6	10.8	407	9	AU087119
C 27	35.6	10.8	465	12	BH169613
C 28	35.6	10.8	506	9	A1117048
C 29	35.6	10.8	528	9	A1119176
C 30	35.6	10.8	541	12	CNS04KUS
C 31	35.6	10.8	720	10	B1683811
C 32	35.4	10.7	500	9	AM200850
C 33	35.4	10.7	644	12	AZ725604
C 34	35.2	10.7	340	10	U92731
C 35	35	10.6	507	12	AZ930800
C 36	35	10.6	640	12	AZ210822
C 37	34.8	10.5	1101	12	CNS00GY6
C 38	34.8	10.5	364	10	BE288646
C 39	34.8	10.5	471	12	AQ638092
C 40	34.8	10.5	495	9	A1388920
C 41	34.8	10.5	548	12	AQ885225
C 42	34.8	10.5	560	9	AM685365
C 43	34.8	10.5	580	9	A1533845
C 44	34.8	10.5	611	9	BE123874
C 45	34.8	10.5	621	10	B1640493

ALIGNMENTS

RESULT 1
LOCUS AU087262/c 500 bp mRNA linear EST 27-JAN-2001
DEFINITION AU087262 Sugano Malaria cDNA library Plasmodium falciparum cDNA
ACCESSION AU087262
VERSION AU087262.1 GI:12389403
KEYWORDS EST.
SOURCE
ORGANISM
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Hemosporidia; Plasmodium.
REFERENCE
Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.
1 (bases 1 to 500)
FULL-LENGTH: a database for a full-length enriched cDNA library
from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
JOURNAL
MEDLINE
COMMENT
Contact: Junichi Watanabe
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
Email: jwatanab@med.s.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..500
/organism="Plasmodium falciparum"
/strain="3D7"
/db_xref="taxon:5833"
/clone="xpp4095"
/clone_lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
BASE COUNT
256 a 41 c 55 g 148 t
ORIGIN

Query Match 12.1%; Score 40; DB 9; Length 500;

Best Local Similarity 49.1%; Pred. NO. 1.2;
Matches 106; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

OY	14	ctccagcggagaaacatctcatcaacactcgcatactgcgaacacttcaggcaaca	73
Db	302	CATTCACCAACCAATTTATTTATTTATTTATTTGTTATTTATTCATTTATTTGTTATTTA	243
OY	74	acatctacatcgctgctgctcagtcgaaacgctgtaaaccttcatactctctcgta	133
Db	242	TTATCATTTATTTATTTGTTATTTATTCACATTTATTTGTTATTTATTCATTTATTTGTTA	183
OY	134	ctactgcttaagctctctcgcgaactgctgttatcaacaatgaagctctctctactactcgct	193
Db	182	TTAAATTTATTTATTTATTTATTCATTTGTTTCATTTTCATTTTCCTTTTCTTATTTATTTGTTG	123
OY	194	tccagctgaacactgcgaactgctactctatcaactc	229
Db	122	TTATTTATTTACTACTATTTAGTACTATTTGTTATTTATTTTC	87

RESULT	2
AA481151/c	
LOCUS	AA481151
DEFINITION	aac4f11.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:615181 3', mRNA sequence.

ACCESSION	AA481151	GI:2210703
VERSION	AA481151.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 565)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 COMMENT

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMUT at:
www-bio.jiml.gov/bbrp/image/image.html
Seq primer: -41m3 fwd. ER from Amersham
High quality sequence stop: 461.

FEATURES	location/qualifiers
source	1. .565

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/organism="Homo sapiens"
/db_xref="GDB:6034169"
/db_xref="taxon:9606"
/clone="IMAGE:815181"
/clone_1lb="NCLCGAP-GCB1"
/lssue_type="germinal center B cell"
/lab_host="DH10B"
/notice="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
CDNA was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staud Marti (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
primed with a Not I - Oligo(dT) primer
15'-GTTACCACATCTGACAGCGAGCGCGCCGTCATCTTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

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ORIGIN

Query Match	11.9%	Score 39.2	DB 9	Length 565
Best Local Similarity	50.5%	Pred. No. 2	1	
Matches	95	Conservative	0	Mismatches 93
				Indels 0
				Gaps 0

Oy aacgctgtaaacacttcatacaactccttcctcgaatactgtaaaagcattcgactggt 159
 Db ATAATGCTATCAGATTCCTATTTTGTCAAGTGCCTGATCACACTTAAATATATGAG 210
 Oy gtatcaacaagaaagttctctctacactcctgtttccgcgtaaacactgacgtacct 219
 Db CTCATTAATCATATATCTATCTGATCCAAACAAAGTTTCTCCCTTACCCCTTACACTTCACA 150
 Oy tctatcactcgcgcgtcggtcccgtaactctctctcgtaactgaactaacactacatcggt 279
 Db CCTACCTTCGCCCTCTCTTAAATATACATCACTAATTAATTTTGAAGAAATTTTACTGCTCTTTT 90

Qy	280	aaatgcga	287
Db	89	AACTGCGA	82

RESULT	3			
LOCUS	BI948321/c			
DEFINITION	BI948321	1014 bp	mRNA	linear EST 19-OCT-2001
	HVSME10009A12f	Hordeum	vulgaris spike	EST library HVCDNA0012

ACCESSION
VERSION
KEYWORDS

(Fusarium Infected) Hordeum vulgare cDNA clone HVSMEI0009A12f, mRNA
sequence.
B1948321
B1948321.1 GI:16288593
EST.

SOURCE	ORGANISM
barley.	<i>Hordeum vulgare</i>
	Eumetazoa: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooidaeae
	1 (bases 1 to 1014)
Wing, R., Muehlbauer, G. J., Close, T. J., Kleinbols, A., Wise, R., Heinemann, R.,	

TITLE	Development of a genetically and physically anchored EST resource for barley genomics: Fusarium Infected Morex spike cDNA library
JOURNAL	Unpublished (2001)
COMMENT	Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twingeclemson.edu
Total hg bases = 153
Seq primer: AATTACCCCTCATTAAAGG
High quality sequence stop: 675.
Location/Qualifiers
1..1014

```

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone_id="HVSME10009A12f"
/clone_lib="Hordeum vulgare spike EST library HVCN0012
(Fusarium infected)"
/issue_type="Spike"
/lab_host="TJ0121"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Plants were grown at the University of Minnesota in
the GJ Muehlbauer lab; spikes were harvested and snap
frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
graminearum inoculation (Helinen). In the TJ Close lab at
the University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all

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Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

High quality sequence stop: 914
Location/Qualifiers

High quality sequence stop: 914
Location/Qualifiers

DB 459 TTTTCACAAATGATATCATGCGTATTTTCTTCTACCTGGTAGAGCTTTCTTGATCAGTCTTTG 400

QY 165 caacatgaacgctctgtctactactcgtctccagctgaacacttgcaactctactat 224
|||||
DB 399 ACACCTTAACATATGATGAGTGCAGCAACACATCATCTGCAGGAGTACTTTCAT 340
|||||

QY 225 caatccgctcgtcgtccgctactctctcgtactgaactaactacatcctcggtta 280
|||||
DB 339 CATTAAGTGACCAACACCTGACCTGTTATCTTGAATTTGCATAAGCTCGCTTCA 284
|||||

RESULT 10
A2729728 558 bp DNA linear GSS 25-JAN-2001
LOCUS RPCI-24-99F3.TV RPCI-24 Mus musculus genomic clone RPCI-24-99F3,
DEFINITION DNA sequence.
ACCESSION A2729728
VERSION A2729728.1 GI:12487775
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 558)
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-99F3.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 99 row: F column: 3
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..558
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-99F3"
/clone_1lb="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site.1: BamHI; Site.2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57Bl/6J
DNA."

BASE COUNT 213 a 90 c 142 g 113 t
ORIGIN

Query Match 11.2%; Score 36.8; DB 12; Length 558;
Best Local Similarity 49.0%; Pred. No. 9.8;
Matches 98; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 74 acctctacatcgttgtgtgcagtcgaacgcttcaacacttcacatctctctgcta 133
|||||
DB 544 ACCTAGGCAATGAGCTTTTCTTCTGAGACTTATGCTGAATAGCTTCCCTTTC 485
|||||

QY 134 ctactgttaagatctatcgtacgctgtgtatcaacatgaacgcttctctactactcgtc 193
|||||

DB 484 TTTCTTTTTCGTAATTCGATGACTGTTGTAACATCGAGGTTTCGGCTCAAACTCCTC 425

QY 194 tccagctgaacacttgcaactctctactcactccgctccgctgcccgtactctctc 253
|||||

DB 424 TCCAGCTGTGATTTATTCCTGCTCTCTGCTTGGCCTCTGTGAATTACTCTGCTT 365
|||||

QY 254 gtactgaactaactacatc 273
|||||

DB 364 GTCCTCATACTACTGATGAC 345
|||||

RESULT 11
A2729405 709 bp DNA linear GSS 25-JAN-2001
LOCUS RPCI-24-99F2.TV RPCI-24 Mus musculus genomic clone RPCI-24-99F2,
DEFINITION DNA sequence.
ACCESSION A2729405
VERSION A2729405.1 GI:12487129
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 709)
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-99F2.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 99 row: F column: 2
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..709
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-99F2"
/clone_1lb="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site.1: BamHI; Site.2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57Bl/6J
DNA."

BASE COUNT 268 a 115 c 176 g 150 t
ORIGIN

Query Match 11.2%; Score 36.8; DB 12; Length 709;
Best Local Similarity 56.7%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 154 actggtgtatcaacatgaacgctctgtctactactcgtctccagctgaacacttgact 213
|||||
DB 469 ACTGACTGTTCAACCTCGAGGTTCTGCTCAAACTCCTCCAAACGTTGTATTAT 410
|||||

QY 214 cgtactctatcactccggtccgctgctactctctcgtactgaactaactaatc 273
|||||

Df	409	CCTGGTTCGTGCTTGAGCCCTCCTTTGAATTAACACTGCATTGCCCACTAACAAGTAGC	350
RESULT_12	AZ161580	428 bp DNA linear GSS 29-AUG-2000	
LOCUS	AZ161580/C		
DEFINITION	SP_0070.AL_E04.SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=70 Col=7 Row=I, DNA sequence.		
ACCESSION	AZ161580		
VERSION	AZ161580.1	GI:8314253.	
SOURCE	GSS.		
ORGANISM	Strongylocentrotus purpuratus. Strongylocentrotus purpuratus. Eukaryote; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinida; Strongylocentrotidae; Strongylocentrotus. 1 (bases 1 to 428) Cameron,R.A., Mahliras,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Foustka,A.D., Livingston,B.T., Wray ,G.A., Ettensohn,C.A., Lehnach,H., Britten,R.J., Davidson,E.H. and Hood,L. A sea urchin genome project: Sequence scan, virtual map, and additional resources Proc.Natl. Acad.Sci.U.S.A. 97 (17), 9514-9518 (2000)		
REFERENCE			
AUTHORS			
TITLE	JOURNAL MEDLINE COMMENT	Contact: Cameron, RA, Davidson, EH, Hood, L Division of Biology 156-29 California institute of technology Pasadena california 91125, USA Tel: (626) 395-8421 Fax: (626) 793-3047 Email: acameron@caltech.edu Plate: 70 row: I column: 7 Seq primer: SP6 Class: BAC ends High quality sequence stop: 428.	
FEATURES	source	location/Qualifiers	
		1..428 /organism="Strongylocentrotus purpuratus" /db_xref="taxon:7668" /clone="plate=70 Col=7 Row=I" /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library" /note="Organ: sperm; Vector: BACe3.6; BAC Clones In E-Coli DH10B"	
BASE COUNT	154 a	47 c	78 g 148 t 1 others
ORIGIN			
Query Match	11.0%; Score 36.4;	DB 12;	Length 428;
Best Local Similarity	52.3%;	Pred.No.11;	
Matches	79;	Conservative 0;	Mismatches 72; Indels 0; Gaps 0;
OY	44	cgaatcatcgaacacctatcgagcaaacatctacatcggtggtgcagtccaac	103
Db	428	CGATCATCATTAATCAATCAATCAATCAATCAATCAATCATCTGCTAGTATCAATCTTATGA	369
OY	104	gtgttaacaacttcatactcttcttgctactacacgtttaagctatctgcacttgttga	163
Db	368	TTATTAAATTATTAATCAATTAATCAATTAATCAATTAATTAATTAATCGTNATAAGTACCATTGA	309
OY	164	tcaacatgaacgtctgctactactactgitt	194
Db	308	TTATTATCATCTCATCACTAGTATTTTATCTT	278
RESULT_13	AQ365154	644 bp DNA linear GSS 16-DEC-1999	
LOCUS	AQ365154		
DEFINITION	nbbd0063C08R CUCI Rice BAC Library Oryza sativa genomic clone nbbd0063C08r, DNA sequence.		
ACCESSION	AQ365154		

[illegible]

RESULT	14
AZ196614	739 bp DNA linear GSS 31-AUG-2000
LOCUS	
DEFINITION	SP_1032_A2-B09.SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1032 Col=18 Row=C, DNA sequence.
ACCESSION	AZ196614
VERSION	AZ196614.1 GI:8390437
KEYWORDS	GSS.
SOURCE	Strongylocentrotus purpuratus.
ORGANISM	Strongylocentrotus purpuratus
REFERENCE	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoidae; Strongylocentroidea; Strongylocentrotus.
AUTHORS	1 (bases 1 to 739) Cameron,R.A., Mahaltras,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
TITLE	A sea urchin genome project: Sequence scan, virtual map, and additional resources
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
MEDLINE	20402566
COMMENT	Contact: Cameron, RA, Davidson, EH, Hood, L Division of Biology 156-29 California Institute of Technology Pasadena California 91125, USA Tel.: (626) 395-8421 Fax: (626) 793-3047 Email: acameron@caltech.edu Plate: 1032 row: C column: 18 Seq primer: SP6 Class: BAC ends High quality sequence stop: 739. Location/Qualifiers 1..739 /organism="Strongylocentrotus purpuratus" /db_xref="taxon:7668" /clone_plate=1032 Col=18 Row=C" /clone_id="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library" /note="Organ: sperm; Vector: BACs.6; BAC clones in E-Coli DH10B"
FEATURES	
source	
BASE COUNT	228 a 131 c 93 g 287 t
ORIGIN	
Query Match	11.0%: Score 36.4; DB 12; Length 739;
Best Local Similarity	48.5%: Pred. No. 14;
Matches 100; Conservative	0; Mismatches 106; Indels 0; Gaps 0;
OY	25 aaacatcatcaacaaccgcgatcctcgtaacacatcatcagaaacaatctacatc 84
Db	317 ATATATTATCATCATGATCATCATCATCAACAACATCGCATTTATGGTATATTATTT 376
OY	85 gttagtggtcagtcgaaacgigttaaacacttcatcatcctcttgcctaactgtaa 144
Db	377 ATTATATTATTATATATAGTACTATCTATCTAAATTTGTATTATATTATTAACGCTAAT 436
OY	145 gcctatcgacctgggttatcaaatgaagtcttgtctactactcgtttccagaactgaa 204
Db	437 TATACTATTACTCCGATTAATTAATCACTCAATTCATATTATTATTACTCTATCAATTA 496
OY	205 actgcgaactcgtaactctacatccc 230
Db	497 ATTACTCTATATTATTAACCATTAATCTCC 522
RESULT	15
AZ841683	561 bp DNA linear GSS 20-FEB-2001
LOCUS	
DEFINITION	ZMO133N17R Mouse 10kb plasmid UDGCM library Mus musculus genomic clone UDGCMO133N17 R, DNA sequence.

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
AZ841683									
AZ841683.1	GI:13011591								
SS.									
house mouse.									
Mus musculus									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
1 (bases 1 to 561)									
Dunn,D., Aoyagi,A., Barber,M., Beaconr,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Petersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.									
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts									
Unpublished (2000)									
Contact: Robert B. Weiss									
University of Utah									
University of Utah									
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT									
84112, USA									
Tel: 801 585 5606									
Fax: 801 585 7177									
Email: ddunn@genetics.utah.edu									
Insert Length: 10000 Std Error: 0.00									
Plate: 0139 row: N column: 17									
Seq primer: CACACAGGAAACACCTATGACC									
Class: plasmid ends									
High quality sequence stop: 561.									
Location/Qualifiers									
1. 561									
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/clone="U08C2M0139N17"									
/clone_id="Mouse 10kb plasmid U08C1M library"									
/sex="Male"									
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"									
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource									
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473211419b1AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."									
BASE COUNT	77 a	138 c	116 g	230 t					
ORIGIN									
Query Match	11.0%;	Score 36.2;	DB 12;	Length 561;					
Best Local Similarity	56.2%;	Pred. No. 14;							
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Db	340	CTCTGGTGTATTCATATTAACTGTCGCTCAAACTCCCTCCAAAGCTGATATCCAA	399						
0Y	213	tcgtactctatcaactcgcgcgtgcgcgtactctctgtactgaataactat	272						
Db	400	TCCTGGCTTGTCTCTCACCAGCTTCTCTGAATGTTCTCTGGCCTCACTACTGTAG	459						
0Y	273	c	273						

Db 460 C 460

Search completed: August 15, 2002, 09:13:06
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